CLAIMS

1.   An RNA sequence analyzer comprising:

a grammar storage unit that stores structural topologies of RNA secondary structures with grammars corresponding to the structural

5   topologies;

a parsing unit that derives parse trees by applying an RNA sequence to the grammars;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit;

10   a sorting unit that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit; and

an output unit that outputs the parse trees sorted by the sorting unit as secondary structure candidates of the RNA sequence.

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2.   An RNA sequence analyzer comprising:

a grammar storage unit that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

20   a parsing unit that derives parse trees by applying RNA sequences to the grammar;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit; and

an output unit that outputs the RNA sequences, from which

25   the parse trees having the goodnesses of fit that satisfy preset conditions are

derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

3.   An RNA sequence analyzer comprising:

a grammar storage unit that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

a parsing unit that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit;

an extraction unit that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation unit that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction unit and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

4.   An RNA sequence analyzer comprising:

a grammar storage unit that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

an RNA sequence production unit that produces RNA sequences transcribed from a DNA sequence input by a user;

a parsing unit that derives parse trees by applying the grammar to the RNA sequences produced by the RNA sequence production

5   unit;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit; and

a gene prediction unit that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the

10   goodnesses of fit that satisfy preset conditions are derived, as gene candidates.

5.   An RNA sequence analyzer comprising:

a grammar storage unit that stores a structural topology of

15   RNA secondary structures with a grammar corresponding to the structural topology;

a parsing unit that derives parse trees by applying the grammar to RNA sequences;

a goodness-of-fit calculation unit that calculates goodnesses

20   of fit of the parse trees derived by the parsing unit; and

a similarity calculation unit that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation unit.

25   6.   An RNA sequence analyzer comprising:

a grammar storage unit that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

a parsing unit that derives parse trees by applying RNA

5 sequences to the grammars;

a goodness-of-fit calculation unit that calculates goodnesses of fit of the parse trees derived by the parsing unit; and

an extraction unit that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset

10 conditions are derived;

a goodness-of-fit matrix creation unit that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the

15 extraction unit and the structural topologies in the two-dimensional matrix; and

a common structure extraction unit that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation unit, that parses other RNA sequences based on the grammar corresponding to an order of the sorted

20 structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.

7.   An RNA sequence analysis method comprising:

25   a grammar storage step that stores structural topologies of

RNA secondary structures with grammars corresponding to the structural topologies;

a parsing step that derives parse trees by applying an RNA sequence to the grammars;

5 a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step;

a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit; and

10 an output step that outputs the parse trees sorted by the sorting step as secondary structure candidates of the RNA sequence.

8. An RNA sequence analysis method comprising:

a grammar storage step that stores a structural topology of 15 RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying RNA sequences to the grammar;

a goodness-of-fit calculation step that calculates goodnesses 20 of fit of the parse trees derived by the parsing step; and

an output step that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

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9.   An RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

5   a parsing step that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step;

an extraction step that extracts the RNA sequences from 10   which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by 15   the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

10.   An RNA sequence analysis method comprising:

20   a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

an RNA sequence production step that produces RNA sequences transcribed from a DNA sequence input by a user;

25   a parsing step that derives parse trees while applying the

grammar to the RNA sequences produced by the RNA sequence production step;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

5   a gene prediction step that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as gene candidates.

10   11.   An RNA sequence analysis method comprising:

a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying the

15   grammar to RNA sequences;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the

20   goodness-of-fit calculation step.

12.   An RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural

25   topologies;

a parsing step that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

5 an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA

10 sequences in a two-dimensional matrix, and which displays the goodnesses of fit on lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix; and

a common structure extraction step that sorts the structural

15 topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse

20 trees having the goodnesses of fit that satisfy the preset conditions.

13. A computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of

25 RNA secondary structures with grammars corresponding to the structural

topologies;

a parsing step that derives parse trees by applying an RNA sequence to the grammars;

a goodness-of-fit calculation step that calculates goodnesses

5   of fit of the parse trees derived by the parsing step;

a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit; and

an output step that outputs the parse trees sorted by the

10   sorting step as secondary structure candidates of the RNA sequence.

14.   A computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores a structural topology of

15   RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying RNA sequences to the grammar;

a goodness-of-fit calculation step that calculates goodnesses

20   of fit of the parse trees derived by the parsing step; and

an output step that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the secondary structures consistent with the structural topology.

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15. A computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

a parsing step that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step;

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA sequences.

16. A computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores a structural topology of RNA secondary structures with a grammars corresponding to the structural topology;

an RNA sequence production step that produces RNA

sequences transcribed from a DNA sequence input by a user;

a parsing step that derives parse trees by applying the grammar to the RNA sequences produced by the RNA sequence production step;

5   a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

a gene prediction step that predicts parts of the DNA sequence corresponding to the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as

10   gene candidates.

17.   A computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores a structural topology of

15   RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying the grammar to RNA sequences;

a goodness-of-fit calculation step that calculates goodnesses

20   of fit of the parse trees derived by the parsing step; and

a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation step.

25   18.   A computer program that makes a computer to execute an

RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

5 a parsing step that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

an extraction step that extracts the RNA sequences from

10 which the parse trees having the goodnesses of fit that satisfy preset conditions are derived;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of

15 fit on lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix; and

a common structure extraction step that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix

20 created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.

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19.   A computer readable recording medium storing a computer program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores a structural topologies of

5   RNA secondary structures with grammars corresponding to the structural topologies;

a parsing step that derives parse trees by applying an RNA sequence to the grammars;

a goodness-of-fit calculation step that calculates goodnesses

10   of fit of the parse trees derived by the parsing step;

a sorting step that sorts the parse trees having the goodnesses of fit that satisfy preset conditions in a descending order of the goodnesses of fit; and

an output step that outputs the parse trees sorted by the

15   sorting step as secondary structure candidates of the RNA sequence.

20.   A computer readable recording medium storing a computer program that makes a computer to execute an RNA sequence analysis method comprising:

20   a grammar storage step that stores a structural topology of RNA secondary structures with a grammar corresponding to the structural topology;

a parsing step that derives parse trees by applying RNA sequences to the grammar;

25   a goodness-of-fit calculation step that calculates goodnesses

of fit of the parse trees derived by the parsing step; and

an output step that outputs the RNA sequences, from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived, as RNA sequence candidates that could potentially form the

5   secondary structures consistent with the structural topology.

21.   A computer readable recording medium storing a computer program that makes a computer to execute an RNA sequence analysis method comprising:

10   a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

a parsing step that derives parse trees by applying RNA sequences to the grammars;

15   a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step;

an extraction step that extracts the RNA sequences from which the parse trees having the goodnesses of fit that satisfy preset conditions are derived; and

20   a common structure matrix creation step that displays the structural topologies and the RNA sequences in a two-dimensional matrix, that gives marks to lattice parts corresponding to the RNA sequences extracted by the extraction step and the structural topologies in the two-dimensional matrix, and that thereby visualizes the structural topologies common to the RNA

25   sequences.

22.   A computer readable recording medium storing a computer

program that makes a computer to execute an RNA sequence analysis

method comprising:

5   a grammar storage step that stores a structural topology of

RNA secondary structures with a grammar corresponding to the structural

topology;

an RNA sequence production step that produces RNA

sequences transcribed from a DNA sequence input by a user;

10   a parsing step that derives parse trees by applying the

grammar to the RNA sequences produced by the RNA sequence production

step;

a goodness-of-fit calculation step that calculates goodnesses

of fit of the parse trees derived by the parsing step; and

15   a gene prediction step that predicts parts of the DNA

sequence corresponding to the RNA sequences, from which the parse trees

having the goodnesses of fit that satisfy preset conditions are derived, as

gene candidates.

20   23.   A computer readable recording medium storing a computer

program that makes a computer to execute an RNA sequence analysis

method comprising:

a grammar storage step that stores a structural topology of

RNA secondary structures with a grammar corresponding to the structural

25   topology;

a parsing step that derives parse trees by applying the grammar to RNA sequences;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

5   a similarity calculation step that calculates a similarity among the RNA sequences based on the goodnesses of fit calculated by the goodness-of-fit calculation step.

24.   A computer readable recording medium storing a computer

10   program that makes a computer to execute an RNA sequence analysis method comprising:

a grammar storage step that stores structural topologies of RNA secondary structures with grammars corresponding to the structural topologies;

15   a parsing step that derives parse trees by applying RNA sequences to the grammars;

a goodness-of-fit calculation step that calculates goodnesses of fit of the parse trees derived by the parsing step; and

an extraction step that extracts the RNA sequences from

20   which the parse trees having the goodnesses of fit that satisfy preset conditions;

a goodness-of-fit matrix creation step that creates a goodness-of-fit matrix which displays the structural topologies and the RNA sequences in a two-dimensional matrix, and which displays the goodnesses of

25   fit on lattice parts corresponding to the RNA sequences extracted by the

extraction step and the structural topologies in the two-dimensional matrix; and

a common structure extraction step that sorts the structural topologies according to the goodnesses of fit for the goodness-of-fit matrix created by the goodness-of-fit matrix creation step, that parses other RNA sequences based on the grammar corresponding to an order of the sorted structural topologies, and obtains the parse trees having optimum goodnesses of fit, and that extracts the other RNA sequences corresponding to the parse trees having the goodnesses of fit that satisfy the preset conditions.